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FIGURE 1

SEQ.ID.NO:1 Sequence of the Codon-Optimized HPV16 L1

ATGAGCCTGTGGCTGCCCAGCGAGGCCACCGTGTACCTGCCTCCCGTGCCCCG
TGAGCAAGGTGGTGAGCACCGACGAGTACGTGGCCCGCACCAACATCTACTA
CCACGCCGGCACCAGCCGCCTGCTGGCCGTGGGCCACCCCTACTTCCCCATC
AAGAAGCCCAACAACAACAAGATCCTGGTGCCCAAGGTGAGCGGCCTGCAG
TACCGCGTGTTCGCGATCCACCTGCCCCGACCCCAACAAGTTCGGCTTCCCCGA
CACAAGCTTCTACAACCCCGACACCCAGCGCCTGGTGTGGGCCTGCGTGGGC
GTGGAGGTGGGCCGCGGCCAGCCCCTGGGCGTGGGCATCAGCGGCCACCCCC
TGCTGAACAAGCTGGACGACACCGAGAACGCCAGCGCCTACGCCGCCAACGC
CGGCGTGGACAACCGCGAGTGCATCAGCATGGACTACAAGCAGACCCAGCTG
TGCCTGATCGGCTGCAAGCCTCCCATCGGCGAGCACTGGGGCAAGGGCAGCC
CCTGCACCAACGTGGCCGTGAACCCCGGCGACTGCCCTCCCCTGGAGCTGAT
CAACACCGTGATCCAGGACGGCGACATGGTGGACACCGGCTTCGGCGCCATG
GACTTCACCACCCTGCAGGCCAACAAGAGCGAGGTGCCCTGGACATCTGCA
CCAGCATCTGCAAGTACCCCGACTACATCAAGATGGTGAGCGAGCCCTACGG
CGACAGCCTGTTCTTCTACCTGCGCCGCGAGCAGATGTTTCGTGCGCCACCTGT
TCAACCGCGCCGCGCCGTGGGCGAGAACGTGCCCGACGACCTGTACATCAA
GGGCAGCGGCAGCACCGCCAACCTGGCCAGCAGCAACTACTTCCCCACTCCC
AGCGGCAGCATGGTGACCAGCGACGCCCAAATCTTCAACAAGCCCTACTGGC
TGCAGCGCGCCCAGGGCCACAACAACGGCATCTGCTGGGGCAACCAGCTGTT
CGTGACCGTGGTGGACACCACCCGCAGCACCAACATGAGCCTGTGCGCCGCC
ATCAGCACCGAGCGAGACCACCTACAAGAACACCAACTTCAAGGAGTACCTGC
GCCACGGCGAGGAGTACGACCTGCAGTTCATCTTCCAGCTGTGCAAGATCAC
CCTGACCGCCGACGTGATGACCTACATCCACAGCATGAACAGCACCATCCTG
GAGGACTGGAACCTTCGGCCTGCAGCCCCCTCCCGGCGGTACCCTGGAGGACA
CCTACCGCTTCGTGACCAGCCAGGCCATCGCCTGCCAGAAGCACACCCCTCC
CGCTCCCAAGGAGGATCCCCTGAAGAAGTACACCTTCTGGGAGGTGAACCTG
AAGGAGAAGTTCAGCGCCGACCTGGACCAGTTCACCCCTGGGGCCGCAAGTTC
TGCTGCAGGCCGGCCTGAAGGCCAAGCCCAAGTTCACCCTGGGCAAGCGCAA
GGCCACCCCCACCACCAGCAGCACCCAGCACCCGCCAAGCGCAAGAAGCG
CAAGCTGTAA

001233 5044360

FIGURE 2

SEQ.ID.NO:2 Codon-Optimized HPV16 E1-G482D,W439R Mutant:

09543105 "092400
007280" 50724960

ATGGCCGACCCCGCCGGCACCAACGGCGAGGAGGGCACCCGGCTGCAACGGC
TGGTTCTACGTGGAGGCCGTGGTGGAGAAGAAGACCGGCGACGCCATCAGCG
ACGACGAGAACGAGAACGACAGCGACACCGGCGAGGACCTGGTGGACTTCA
TCGTGAACGACAACGACTACCTGACCCAGGCCGAGACCGAGACCGCCACGCG
CCTGTTACCGCCCAGGAGGCCAAGCAGCACCGCGACGCCGTGCAGGTGCTG
AAGCGCAAGTACCTGGGCAGCCCCCTGAGCGACATCAGCGGCTGCGTCGACA
ACAACATCAGCCCCCGCCTGAAGGCCATCTGCATCGAGAAGCAGAGCCGCGC
CGCCAAGCGCCGCTGTTCGAGAGCGAGGACAGCGGCTACGGCAACACCGA
GGTGGAGACCCAGCAGATGCTGCAGGTGGAGGGCCGCCACGAGACCGAGAC
CCCCTGCAGCCAGTACAGCGGCGGCAGCGGCGGCGGCTGCAGCCAGTACAGC
AGCGGCAGCGGCGGCGAGGGCGTGAGCGAGCGCCACACCATCTGCCAGACC
CCTCTGACCAACATCCTGAACGTGCTGAAGACCAGCAACGCCAAGGCCGCCA
TGCTGGCCAAGTTCAAGGAGCTGTACGGCGTGAGCTTCAGCGAGCTGGTGC
CCCCTTCAAGAGCAACAAGAGCACCTGCTGCGACTGGTGCATCGCCGCTTC
GGCCTGACCCCCAGCATCGCCGACAGCATCAAGACCCTGCTGCAGCAGTACT
GCCTGTACCTGCACATCCAGAGCCTGGCCTGCAGCTGGGGCATGGTGGTGCT
GCTGCTGGTGCCTACAAGTGCGGCAAGAACCGCGAGACCATCGAGAAGCTG
CTGAGCAAGCTGCTGTGCGTGAGCCCCATGTGCATGATGATCGAGCCTCCCA
AGCTTCGCAGCACCCGCCGCCCTGTACTGGTACAAGACCGGCATCAGCAA
CATCAGCGAGGTGTACGGCGACACCCCCGAGTGGATCCAGCGCCAGACCGTG
CTGCAGCACAGCTTCAACGACTGCACCTTCGAGCTGAGCCAGATGGTGCAGT
GGGCCTACGACAACGACATCGTGGACGACAGCGAGATCGCCTACAAGTACGC
CCAGCTGGCCGACACCAACAGCAACGCCAGCGCCTTCCTGAAGAGCAACAGC
CAGGCCAAGATCGTGAAGGACTGCGCCACCATGTGCCGCCACTACAAGCGCG
CCGAGAAGAAGCAGATGAGCATGAGCCAGTGGATCAAGTACCGCTGCGACC
GCGTGACGACGGCGGCGACCGCAAGCAGATCGTGATGTTCTGCGCTACCA
GGGCGTGGAATTCATGAGCTTCCTGACCGCCCTGAAGCGCTTCCTGCAGGGC
ATCCCCAAGAAGAAGTGCATCCTGCTGTACGGCGCCGCCAACACCGACAAGA
GCCTGTTTCGGCATGAGCCTGATGAAGTTCCTGCAGGGCAGCGTGATCTGCTTC
GTGAACAGCAAGAGCCACTTCTGGCTGCAGCCCCTGGCCGACGCCAAGATCG
GCATGCTGGACGACGCCACCGTGCCCTGCTGGAACTACATCGACGACAACCT
GCGCAACGCCCTGGACGGCAACCTGGTGAGCATGGACGTGAAGCACCGCCCC
CTGGTGCAGCTGAAGTGCCCTCCCCTGCTGATCACCAGCAACATCAACGCCG
GCACCGACAGCCGCTGGCCCTACCTGCACAACCGCCTGGTGGTGTTACCTTC
CCCAACGAGTTCCCCTTCGACGAGAACGGTAACCCCGTGACGAGCTGAACG
ACAAGAAGTGAAGAGCTTCTTCAGCCGCACCTGGAGCCGCTGAGCCTGCA
CGAGGACGAGGACAAGGAGAACGACGGCGACAGCCTGCCCACCTTCAAGTG
CGTGAGCGGCCAGAACCAACACCCTGTAA

FIGURE 3

SEQ.ID.NO.:3 Sequence of the Codon-Optimized HPV16E2-E39A,I73A Mutant:

ATGGAGACCCTGTGCCAGCGCCTGAACGTGTGCCAGGACAAGATCCTGACCC
ACTACGAGAACGACAGCACCGACCTGCGCGACCACATCGACTACTGGAAGCA
CATGCGCCTGGCCTGCGCCATCTACTACAAGGCCCGCGAGATGGGCTTCAAG
CACATCAACCACCAGGTGGTGCCACCCTGGCCGTGAGCAAGAACAAGGCCC
TGCAGGCCCGCCGAGCTGCAGCTGACCCTGGAGACCATCTACAACAGCCAGTA
CAGCAACGAGAAGTGGACCCTGCAGGACGTGAGCCTGGAGGTGTACCTGACC
GCCCCCACC GGCTGCATCAAGAAGCACGGCTACACCGTGGAGGTGCAGTTCG
ACGGCGACATCTGCAACACCATGCACTACACCAACTGGACCCACATCTACAT
CTGCGAGGAGGCCAGCGTGACCGTGGTGGAGGGCCAGGTGGACTACTACGG
CCTGTACTACGTGCACGAGGGCATCCGCACCTACTTCGTGCAGTTCAAGGAC
GACGCCGAGAAGTACAGCAAGAACAAGGTGTGGGAGGTGCACGCCGGCGGC
CAGGTGATCCTGTGCCCCACCAGCGTGTTCAGCAGCAACGAGGTGAGCAGCC
CCGAGACCATCCGCCAGCACCTGGCCAACCACAGCGCCGCCACCCACACCAA
GGCCGTGGCCCTGGGCACCGAGGAGACCCAGACCACCATCCAGCGCCCCCGC
AGCGAGCCCGACACCGGCAACCCCTGCCACACCACCAAGCTGCTGCACCGCG
ACAGCGTGGACAGCGCCCCCATCCTGACCGCCTTCAACAGCAGCCACAAGGG
CCGCATCAACTGCAACAGCAACACCACCCCATCGTGCACCTGAAGGGCGAC
GCCAACACCCTGAAGTGCCTGCGCTACCGCTTCAAGAAGCACTGCAAGCTGT
ACACCGCCGTGAGCAGCACCTGGCACTGGACCGGCCACAACGTGAAGCACA
AGAGCGCCATCGTGACCCTGACCTACGACAGCGAGTGGCAGCGCGACCAAGTT
CCTGAGCCAGGTGAAGATCCCCAAGACCATCACCGTGAGCACCGGCTTCATG
AGCATCTAA

09642405-092400

FIGURE 4

SEQ.ID.NO.:4 Codon-Optimized HPV16E7-C24G,E26G Mutant:

ATGCACGGCGACACCCCCACCCTGCACGAGTACATGCTGGACCTGCAGCCCG
AGACCACCGACCTGTACGGCTACGGCCAGCTGAACGACAGCAGCGAGGAGG
AGGACGAGATCGACGGCCCCGCCGGCCAGGCCGAGCCCGACCGCGCCCCACT
ACAACATCGTGACCTTCTGCTGCAAGTGCGACAGCACCCCTGCGCCTGTGCGT
GCAGAGCACCCACGTGGACATCCGCACCCTGGAGGACCTGCTGATGGGCACC
CTGGGCATCGTGTGCCCCATCTGCAGCCAGAAGCCCTAA

05642405 0004100

FIGURE 5

SEQ.ID.NO.:5 Codon-Optimized HPV6a E7 Gene:

ATGCACGGCCGCCACGTGACCCTGAAGGACATCGTGCTGGACCTGCAGCCTC
CCGACCCCGTGGGCCTGCACTGCTACGAGCAGCTGGTGGACAGCAGCGAGGA
CGAGGTGGACGAGGTGGACGGCCAGGACAGCCAGCCCCTGAAGCAGCACTT
CCAGATCGTGACCTGCTGCTGCGGCTGCGACAGCAACGTGCGCCTGGTGGTG
CAGTGCACCGAGACCGACATCCGCGAGGTGCAGCAGCTCCTGCTGGGTACCC
TGAACATCGTGTGCCCCATCTGCGCTCCCAAGACCTAA

007280" 50424950

FIGURE 6

SEQ.ID.NO.:6 Codon-Optimized HPV18 E7 Gene:

ATGCACGGCCCCAAGGCCACCCTGCAGGACATCGTGCTGCACCTGGAGCCCC
AGAACGAGATCCCCGTGGACCTGCTGTGCCACGAGCAGCTGAGCGACAGCGA
GGAGGAGAACGACGAGATCGACGGCGTGAACCACCAGCACCTGCCCCGCTCG
CAGGGCCGAGCCCCAGCGCCACACCATGCTGTGCATGTGCTGCAAGTGCGAG
GCCCGCATCGAGCTGGTGGTGGAGAGCAGCGCTGACGACCTGCGCGCCTTCC
AGCAGCTGTTCTGAACACCCTGAGCTTCGTGTGCCCTGGTGCGCCAGCCAG
CAGTAA

007250" 50424960

FIGURE 7

SEQ.ID.NO.:7 Codon-Optimized HPV6a E2 Gene:

ATGGAGGCCATCGCCAAGCGCCTGGACGCCTGCCAGGAGCAGCTGCTGGAGC
TGTACGAGGAGAACAGCACCGACCTGCACAAGCACGTGCTGCACTGGAAGTG
CATGCGCCACGAGAGCGTGCTGCTGTACAAGGCCAAGCAGATGGGCCTGAGC
CACATCGGCATGCAGGTGGTGCCTCCTCTGAAGGTGAGCGAGGCCAAGGGCC
ACAACGCCATCGAGATGCAGATGCACCTCGAGAGCCTGCTGCGCACCGAGTA
CAGCATGGAGCCCTGGACCCTGCAGGAGACCAGCTACGAGATGTGGCAGACC
CCTCCCAAGCGCTGCTTCAAGAAGCGCGGCAAGACCGTGGAGGTGAAGTTCG
ACGGCTGCGCCAACAACACCATGGACTACGTGGTGTGGACCGACGTGTACGT
GCAGGACAACGACACCTGGGTGAAGGTGCACAGCATGGTGGACGCCAAGGG
CATCTACTACACCTGTGGCCAGTTCAAGACCTACTACGTGAACTTCGTGAAGG
AGGCCGAGAAAGTACGGCAGCACCAAGCACTGGGAGGTGTGCTACGGCAGCA
CCGTGATCTGCAGCCCCGCTAGCGTGAGCAGCACCAACCCAGGAGGTGAGCAT
CCCCGAGAGCACCACTACACTCCCGCCCAGACCAGCACCTGCTGAGCAGC
AGCACCAAGGAGGACGCCGTGCAGACCCCTCCTCGCAAGCGCGCCCCGCGGC
GTGCAGCAGAGCCCCTGCAACGCCCTGTGCGTGGCCCACATCGGCCCCGTGG
ATAGCGGCAACCACAACCTGATCACCAACAACCACGACCAGCACCAAGCGCC
GCAACAACAGCAACAGCAGCGCCACTCCCATCGTGCAGTTCCAGGGCGAGAG
CAACTGCCTGAAGTGCTTCCGCTACCGCCTGAACGATCGCCACCGCCACCTGT
TCGACCTGATCAGCAGCACCTGGCACTGGGCCAGCAGCAAGGCTCCCCACAA
GCACGCCATCGTGACCGTGACCTACGACAGCGAGGAGCAGCGCCAGCAGTTC
CTGGACGTGGTGAAGATCCCTCCCACCATCAGCCACAAGCTGGGCTTCATGA
GCCTGCACCTGCTGTAA

004280-504280

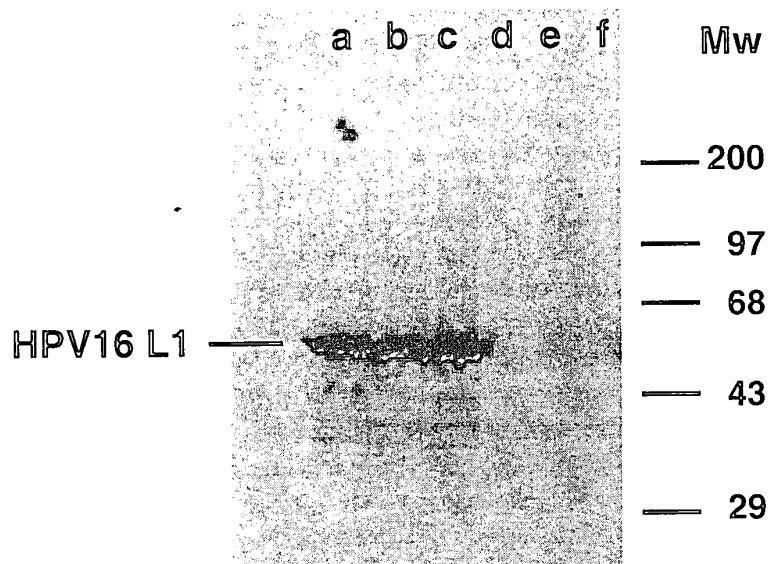
FIGURE 8

SEQ.ID.NO.:8 Codon-Optimized HPV18 E2 Gene:

ATGCAGACTCCCAAGGAGACCCTGAGCGAGCGCCTGAGCGCCCTGCAGGACA
AGATCATCGACCACTACGAGAACGACAGCAAGGACATCGACAGCCAGATCC
AGTACTGGCAGCTGATCCGCTGGGAGAACGCCATCTTCTTCGCCGCTCGCGA
GCACGGGATCCAGACCCTGAACCACCAGGTGGTGCCCCGCCTACAACATCAGC
AAGAGCAAGGCCCAACAAGGCCATCGAGCTGCAGATGGCCCTGCAGGGCCTG
GCCAGAGCGCCTACAAGACCGAGGACTGGACCCTGCAGGACACCTGCGAG
GAGCTGTGGAACACCGAGCCACCCACTGCTTCAAGAAGGGAGGCCAGACC
GTGCAGGTGTACTTCGACGGCAACAAGGACAACCTGCATGAACTACGTGGCCT
GGGACAGCGTGTACTACATGACCGACGCCGGCACCTGGGACAAGACCGCCAC
CTGCGTGAGCCACCGCGGCCTGTACTACGTGAAGGAGGGCTACAACACCTTC
TACATCGAGTTCAAGAGCGAGTGCAGAGAAGTACGGCAACACCGGCACCTGG
GAGGTGCACTTCGGCAACAACGTGATCGACTGCAACGACAGCATGTGCAGCA
CCAGCGACGACACCGTGAGCGCCACCCAGCTGGTGAAGCAGCTGCAGCACAC
TCCCAGCCCCTACAGCAGCACCGTGAGCGTGGGCACCGCCAAGACCTACGGC
CAGACCAGCGCCGCCACTCGCCCTGGCCACTGCGGCCTGGCCGAGAAGCAGC
ACTGCGGGCCCGTGAACCCTCTGCTGGGCGCCGCCACCGCCACCGGCAACAA
CAAGCGCCGCAAGCTGTGCAGCGGCAACACCACTCCCATCATCCACCTGAAG
GGCGACCGCAACAGCCTGAAGTGCCTGCGGTACCGCCTGCGCAAGCACAGCG
ACCACTACCGCGACATCAGCAGCACCTGGCACTGGACCGGCGCCGGGAACGA
GAAGACCGGCATCCTGACCGTGACCTACCACAGCGAGACCCAGCGCACCAAG
TTCCTGAACACCGTGGCCATCCCCGACAGCGTGCAGATCCTGGTGGGCTACA
TGACCATGTAA

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FIGURE 9.
Comparison of protein expression of
native and synthetic HPV16 L1 genes



007280 50424960

[illegible]

HPV 16 E1 —

— 188

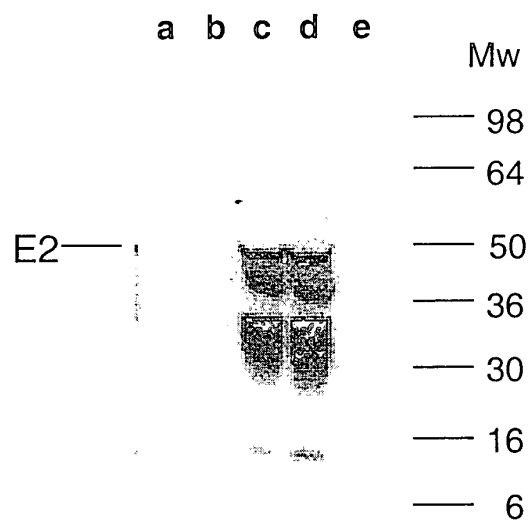
— 97

— 52

33

21

FIGURE 11.

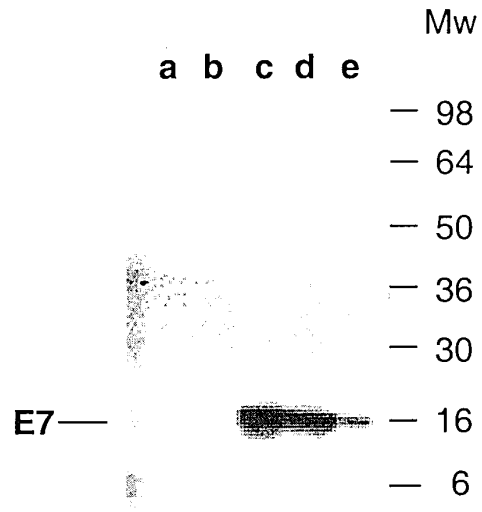


- a. mock
- b. lacZ
- c. synthetic 16 E2 isolate 6
- d. synthetic 16 E2 isolate 11
- e. native 16 E2

xmw98.75 16557-27

FIGURE 12

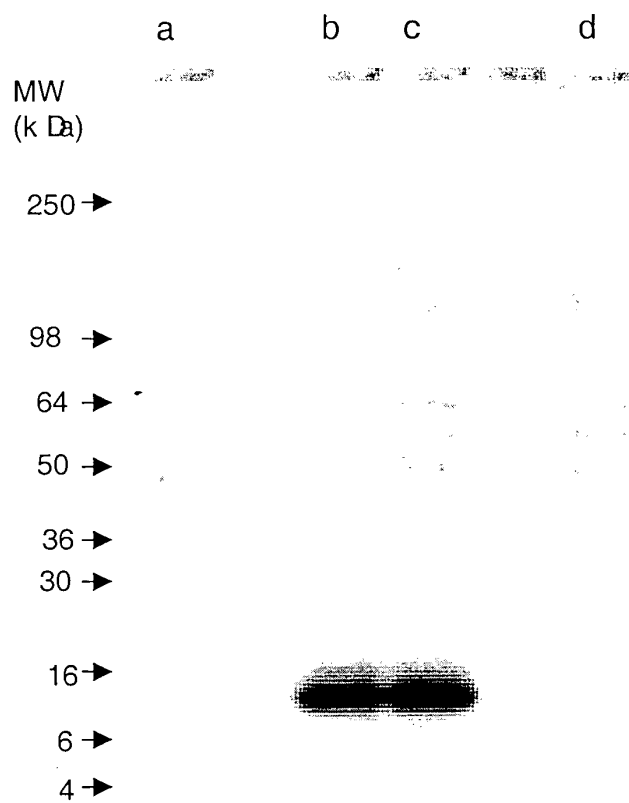
Comparison of protein expression of native and synthetic HPV16 E7 genes



- a. mock
- b. lacZ
- c. synthetic HPV16 E7 isolate 2
- d. synthetic HPV16 E7 isolate 4
- e. native HPV16 E7

xmw98.75 16557-27

FIGURE 13



004230 504490

FIGURE 14

MW
(kDa)

a b c d e f

250 →

98 →

64 →

50 →

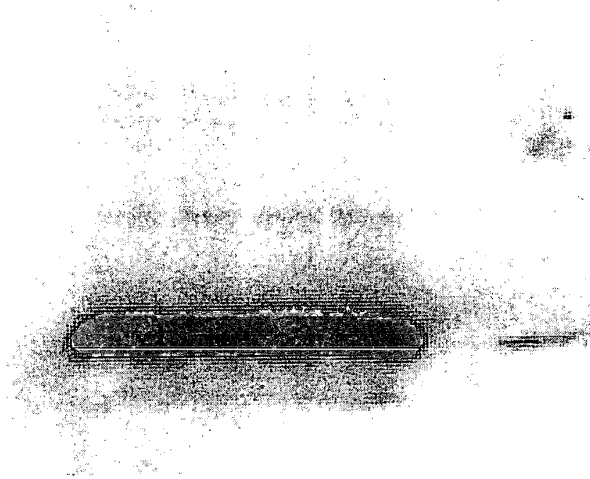
36 →

30 →

16 →

6 →

4 →



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Expression of synthetic HPV 6 E2 gene

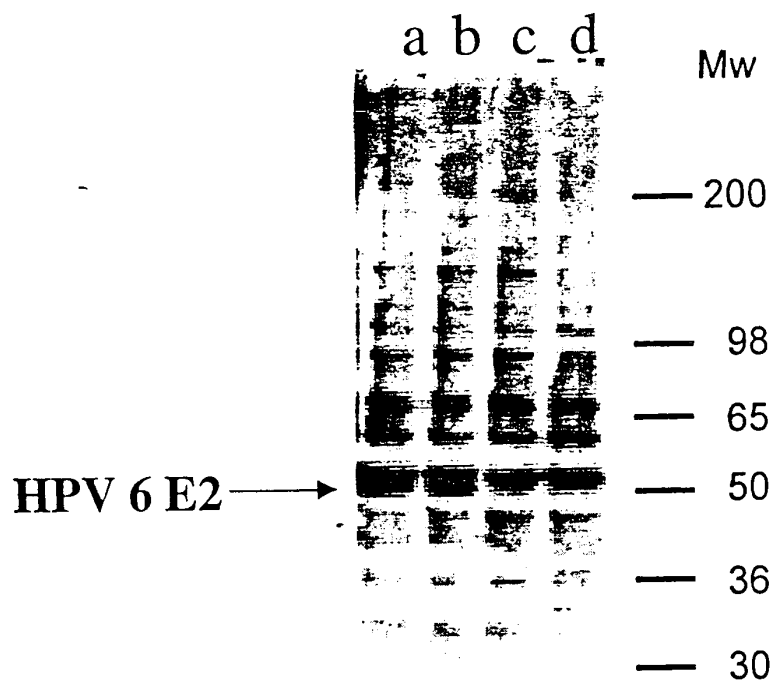


Figure 15. Expression of a synthetic gene encoding HPV 6 E2 protein. 293 cells were transfected with synthetic HPV 6 E2 or control plasmids or were mock transfected. Cell lysates were prepared 48 hr. later, fractionated by SDS PAGE and analyzed by immunoblotting using a goat anti-6E2 antiserum as first antibody. a. 6 E2-5.4; b. 6E2-5.5; c. beta-gal; d. mock.

Expression of synthetic HPV 18 E2 gene

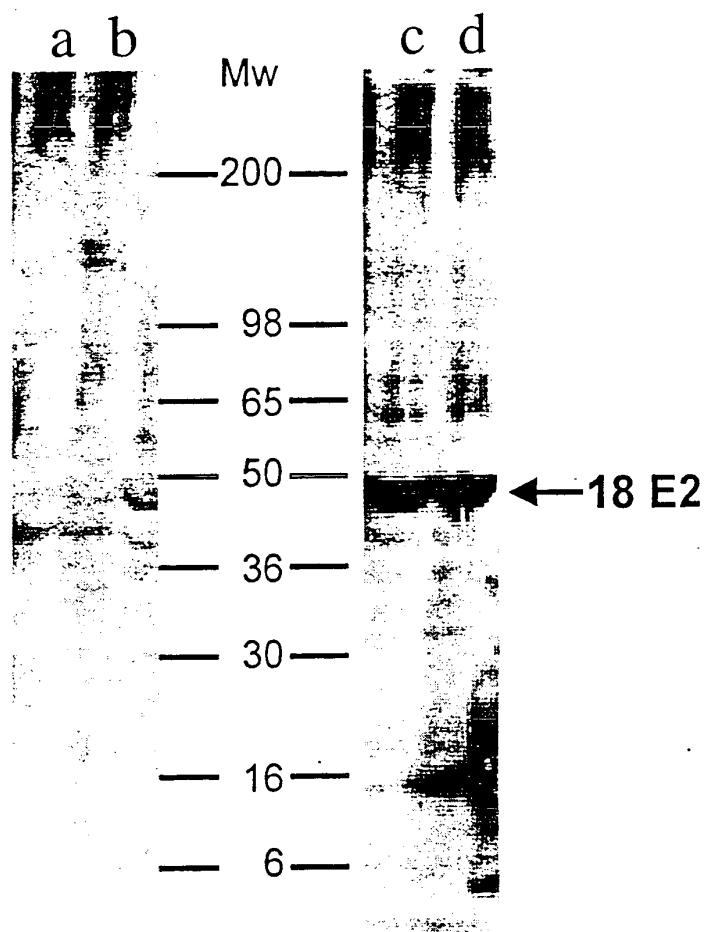


Figure 16. Expression of a synthetic gene encoding HPV 18 E2 protein. 293 cells were transfected with synthetic HPV 18 E2 or control plasmids or were mock transfected. Cell lysates were prepared 48 hr. later, fractionated by SDS PAGE and analyzed by immunoblotting using a goat anti- 18E2 antiserum as first antibody. a. beta-gal; b. mock; c. 18 E2-4.4; d. 18E2-4.5.

FIGURE 17

HPV16 L1 Gene-Building Oligomers

MN4A1 (SEQ.ID.NO:9) 5' ATG AGC CTG TGG CTG CCC AGC GAG GCC ACC
GTG TAC CTG CCT CCC GTG CCC GTG AGC AAG GTG GTG AGC ACC GAC
GAG TAC GTG GCC CGC ACC AAC ATC TAC TAC CAC GCC GGC ACC AGC
CGC CTG CTG 3'

MN4A3 (SEQ.ID.NO:10) 5' CGC ATC CAC CTG CCC GAC CCC AAC AAG TTC
GGC TTC CCC GAC ACA AGC TTC TAC AAC CCC GAC ACC CAG CGC CTG
GTG TGG GCC TGC GTG GGC GTG GAG GTG GGC CGC GGC CAG CCC CTG
GGC GTG GGC 3'

MN4A5 (SEQ.ID.NO:11) 5' GAG TGC ATC AGC ATG GAC TAC AAG CAG ACC
CAG CTG TGC CTG ATC GGC TGC AAG CCT CCC ATC GGC GAG CAC TGG
GGC AAG GGC AGC CCC TGC ACC AAC GTG GCC GTG AAC CCC GGC GAC
TGC CCT CCC 3'

MN4A7 (SEQ.ID.NO:12) 5' GCC AAC AAG AGC GAG GTG CCC CTG GAC ATC
TGC ACC AGC ATC TGC AAG TAC CCC GAC TAC ATC AAG ATG GTG AGC
GAG CCC TAC GGC GAC AGC CTG TTC TTC TAC CTG CGC CGC GAG CAG
ATG TTC GTG CGC 3'

MN4A9 (SEQ.ID.NO:13) 5' GCC AGC AGC AAC TAC TTC CCC ACT CCC AGC
GGC AGC ATG GTG ACC AGC GAC GCC CAA ATC TTC AAC AAG CCC TAC
TGG CTG CAG CGC GCC CAG GGC CAC AAC AAC GGC ATC TGC TGG GGC
AAC CAG CTG 3'

MN4A11 (SEQ.ID.NO:14) 5' GAG TAC CTG CGC CAC GGC GAG GAG TAC GAC
CTG CAG TTC ATC TTC CAG CTG TGC AAG ATC ACC CTG ACC GCC GAC
GTG ATG ACC TAC ATC CAC AGC ATG AAC AGC ACC ATC CTG GAG GAC
TGG AAC TTC GGC CTG 3'

MN4A13 (SEQ.ID.NO:15) 5' GCT CCC AAG GAG GAT CCC CTG AAG AAG TAC
ACC TTC TGG GAG GTG AAC CTG AAG GAG AAG TTC AGC GCC GAC CTG
GAC CAG TTC CCC CTG GGC CGC AAG TTC CTG CTG CAG GCC GGC CTG
AAG GCC AAG CCC AAG 3'

MN4A2 (SEQ.ID.NO:16) 5' GTT GGG GTC GGG CAG GTG GAT GCG GAA CAC
GCG GTA CTG CAG GCC GCT CAC CTT GGG CAC CAG GAT CTT GTT GTT
GTT GGG CTT CTT GAT GGG GAA GTA GGG GTG GCC CAC GGC CAG CAG
GCG GCT GGT GCC GGC 3'

FIG. 17, CTD. 2/3

MN4A4 (SEQ.ID.NO:17) 5' CTT GTA GTC CAT GCT GAT GCA CTC GCG GTT
GTC CAC GCC GGC GTT GGC GGC GTA GGC GCT GGC GTT CTC GGT GTC
GTC CAG CTT GTT CAG CAG GGG GTG GCC GCT GAT GCC CAC GCC CAG
GGG CTG GCC GCG 3'

MN4A6 (SEQ.ID.NO:18) 5' CAG GGG CAC CTC GCT CTT GTT GGC CTG CAG
GGT GGT GAA GTC CAT GGC GCC GAA GCC GGT GTC CAC CAT GTC GCC
GTC CTG GAT CAC GGT GTT GAT CAG CTC CAG GGG AGG GCA GTC GCC
GGG GTT CAC 3'

MN4A8 (SEQ.ID.NO:19) 5' GGG AGT GGG GAA GTA GTT GCT GCT GGC CAG
GTT GGC GGT GCT GCC GCT GCC CTT GAT GTA CAG GTC GTC GGG CAC
GTT CTC GCC CAC GGC GCC GGC GCG GTT GAA CAG GTG GCG CAC GAA
CAT CTG CTC GCG 3'

MN4A10 (SEQ.ID.NO:20) 5' CTC CTC GCC GTG GCG CAG GTA CTC CTT GAA
GTT GGT GTT CTT GTA GGT GGT CTC GCT GGT GCT GAT GGC GGC GCA
CAG GCT CAT GTT GGT GCT GCG GGT GGT GTC CAC CAC GGT CAC GAA
CAG CTG GTT GCC CCA GCA GAT GCC 3'

MN4A12 (SEQ.ID.NO:21) 5' CTT CAG GGG ATC CTC CTT GGG AGC GGG AGG
GGT GTG CTT CTG GCA GGC GAT GGC CTG GCT GGT CAC GAA GCG GTA
GGT GTC CTC CAG GGT ACC GCC GGG AGG GGG CTG CAG GCC GAA GTT
CCA GTC CTC CAG 3'

MN4A14 (SEQ.ID.NO:22) 5' CAC TAG AGA TCT GAA TTC TTA CAG CTT GCG
CTT CTT GCG CTT GGC GGT GGT GCT GGT GCT GCT GGT GGT GGG GGT
GGC CTT GCG CTT GCC CAG GGT GAA CTT GGG CTT GGC CTT CAG GCC
GGC 3'

MN595 (SEQ.ID.NO:23) 5' CGC GGC CAG CCC CTG GGC GTG 3'

MN596 (SEQ.ID.NO:24) 5' GCC CAC GCC CAG GGG CTG GCC GCG 3'

MN597 (SEQ.ID.NO:25) 5' GCC AAC AAG AGC GAG GTG CCC 3'

MN598 (SEQ.ID.NO:26) 5' CAG GGG CAC CTC GCT CTT GTT GGC 3'

MN599 (SEQ.ID.NO:27) 5' GCC AGC AGC AAC TAC TTC CCC AC 3'

MN600 (SEQ.ID.NO:28) 5' GGG AGT GGG GAA GTA GTT GCT GC 3'

001230 50424960

FIG. 17, CTD. 3/3

MN601 (SEQ.ID.NO:29) 5' CTG GAG GAC TGG AAC TTC GGC CTG 3'

MN602 (SEQ.ID.NO:30) 5' CAG GCC GAA GTT CCA GTC CTC CAG 3'

MN603 (SEQ.ID.NO:31) 5' CAC TAG AGA TCT GAA TTC TTA CAG C 3'

MN604 (SEQ.ID.NO:32) 5' CAT CTC AGA TCT GCC ACC ATG AGC CTG TGG
CTG CCC AG 3'

007220" 50424920

FIGURE 18

HPV16E1 Gene-building Oligomers

MN605 (SEQ.ID.NO:33) 5' ATG GCC GAC CCC GCC GGC ACC AAC GGC GAG
GAG GGC ACC GGC TGC AAC GGC TGG TTC TAC GTG GAG GCC GTG GTG
GAG AAG AAG ACC GGC GAC GCC ATC AGC GAC GAC GAG AAC GAG AAC
GAC AGC GAC 3'

MN606 (SEQ.ID.NO:34) 5' GTG CTG CTT GGC CTC CTG GGC GGT GAA CAG
GGC GTG GGC GGT CTC GGT CTC GGC CTG GGT CAG GTA GTC GTT GTC
GTT CAC GAT GAA GTC CAC CAG GTC CTC GCC GGT GTC GCT GTC GTT
CTC GTT CTC GTC 3'

MN607(SEQ.ID.NO:35) 5' GCC CAG GAG GCC AAG CAG CAC CGC GAC GCC
GTG CAG GTG CTG AAG CGC AAG TAC CTG GGC AGC CCC CTG AGC GAC
ATC AGC GGC TGC GTC GAC AAC AAC ATC AGC CCC CGC CTG AAG GCC
ATC TGC ATC GAG 3'

MN608 (SEQ.ID.NO:36) 5' CTC GTG GCG GCC CTC CAC CTG CAG CAT CTG
CTG GGT CTC CAC CTC GGT GTT GCC GTA GCC GCT GTC CTC GCT CTC GAA
CAG GCG GCG CTT GGC GGC GCG GCT CTG CTT CTC GAT GCA GAT GGC
CTT CAG GC 3'

MN609 (SEQ.ID.NO:37) 5' CAG GTG GAG GGC CGC CAC GAG ACC GAG ACC
CCC TGC AGC CAG TAC AGC GGC GGC AGC GGC GGC GGC TGC AGC CAG
TAC AGC AGC GGC AGC GGC GGC GAG GGC GTG AGC GAG CGC CAC ACC
ATC TGC CAG ACC 3'

MN610 (SEQ.ID.NO:38): 5' CTT GAA GGG GCG CAC CAG CTC GCT GAA GCT
CAC GCC GTA CAG CTC CTT GAA CTT GGC CAG CAT GGC GGC CTT GGC
GTT GCT GGT CTT CAG CAC GTT CAG GAT GTT GGT CAG AGG GGT CTG
GCA GAT GGT GTG GCG 3'

MN611 (SEQ.ID.NO:39) 5' GAG CTG GTG CGC CCC TTC AAG AGC AAC AAG
AGC ACC TGC TGC GAC TGG TGC ATC GCC GCC TTC GGC CTG ACC CCC
AGC ATC GCC GAC AGC ATC AAG ACC CTG CTG CAG CAG TAC TGC CTG
TAC CTG CAC ATC CAG 3'

MN612 (SEQ.ID.NO:40) 5' CAT GGG GCT CAC GCA CAG CAG CTT GCT CAG
CAG CTT CTC GAT GGT CTC GCG GTT CTT GCC GCA CTT GTA GCG CAC
CAG CAG CAG CAC CAC CAT GCC CCA GCT GCA GGC CAG GCT CTG GAT
GTG CAG GTA CAG GCA G 3'

007200 00424960

[illegible]

MN620 (SEQ.ID.NO:48) 5' GAA CTC GTT GGG GAA GGT GAA CAC CAC CAG
GCG GTT GTG CAG GTA GGG CCA GCG GCT GTC GGT GCC GGC GTT GAT
GTT GCT GGT GAT CAG CAG GGG AGG GCA CTT CAG CTG CAC CAG GGG
GCG GTG CTT CAC 3'

FIGURE 18, CTD 3/3

MN621 (SEQ.ID.NO:49) 5' GTG TTC ACC TTC CCC AAC GAG TTC CCC TTC
GAC GAG AAC GGT AAC CCC GTG TAC GAG CTG AAC GAC AAG AAC TGG
AAG AGC TTC TTC AGC CGC ACC TGG AGC CGC CTG AGC CTG CAC GAG
GAC GAG 3'

MN623 (SEQ.ID.NO:51) 5' GCC TGA AGG CCA TCT GCA TCG AG 3'

MN625 (SEQ.ID.NO:53) 5' GAG CTG GTG CGC CCC TTC AAG 3'

MN627 (SEQ.ID.NO:55) 5' CTG CTG TGC GTG AGC CCC ATG 3'

MN629 (SEQ.ID.NO:57) 5' GCC ACC ATG TGC CGC CAC TAC 3'

MN631 (SEQ.ID.NO:59) 5' CTG GCC GAC GCC AAG ATC GGC 3'

MN633 (SEQ.ID.NO:61) 5' GTG TTC ACC TTC CCC AAC GAG TTC 3'

MN635 (SEQ.ID.NO:63) 5' CAT GAG AGA TCT TTA CAG GGT GTT G 3'

FIGURE 19

Oligonucleotides used in the generation of synthetic HPV 16 E2

13856-307-2A (SEQ.ID.NO:65) 5' ATG GAG ACC CTG TGC CAG CGC CTG AAC
GTG TGC CAG GAC AAG ATC CTG ACC CAC TAC GAG AAC GAC AGC ACC
GAC CTG CGC GAC CAC ATC GAC TAC TGG 3'

13856-307-2C (SEQ.ID.NO:66) 5' CCA CCA GGT GGT GCC CAC CCT GGC CGT
GAG CAA GAA CAA GGC CCT GCA GGC CGC CGA GCT GCA GCT GAC CCT
GGA GAC GAT CTA CAA CAG CCA GTA CAG CAA CG 3'

13856-307-2E (SEQ.ID.NO:67) 5' CCG GCT GCA TCA AGA AGC ACG GCT ACA
CCG TGG AGG TGC AGT TCG ACG GCG ACA TCT GCA ACA CCA TGC ACT
ACA CCA ACT GGA CCC ACA TTT ACA TCT GTG AGG AGG 3'

13856-307-2G (SEQ.ID.NO:68) 5' CGT GCA CGA GGG GAT CCG CAC CTA CTT
CGT GCA GTT CAA GGA CGA CGC CGA GAA GTA CAG CAA GAA CAA GGT
GTG GGA GGT GCA CGC CGG AGG CCA GGT GAT CC 3'

13856-307-2I (SEQ.ID.NO:69) 5' GGC CAA CCA CAG CGC CGC CAC CCA CAC
CAA GGC CGT GGC CCT GGG CAC CGA GGA GAC CCA GAC CAC AAT CCA
GCG CCC TCG CAG CGA GCC CGA CAC CGG CAA CCC CTG CC 3'

13856-307-2K (SEQ.ID.NO:70) 5' GCC ACA AGG GCC GGA TCA ACT GCA ACA
GCA ACA CCA CCC CTA TCG TGC ACC TGA AGG GCG ACG CCA ACA CCC
TGA AGT GCC TGC GGT ACC GCT TCA AGA AGC ACT GC 3'

13856-307-2B (SEQ.ID.NO:71) 5' CCA GGG TGG GCA CCA CCT GGT GGT TGA
TGT GCT TGA AGC CCA TCT CGC GGG CCT TGT AGT AGA TGG CGC AGG
CCA GGC GCA TGT GCT TCC AGT AGT CGA TGT GGT CGC GCA GG 3'

13856-307-2D (SEQ.ID.NO:72) 5' GCC GTG CTT CTT GAT GCA GCC GGT AGG
GGC GGT CAG GTA CAC CTC CAG GCT CAC GTC CTG CAG GGT CCA CTT
CTC GTT GCT GTA CTG GCT GTT GTA GAT CG 3'

13856-307-2F (SEQ.ID.NO:73) 5' GGT GCG GAT CCC CTC GTG CAC GTA GTA
CAG GCC GTA GTA GTC CAC CTG GCC CTC CAC CAC GGT CAC GCT GGC
CTC CTC ACA GAT GTA AAT GTG GGT CC 3'

13856-307-2H (SEQ.ID.NO:74) 5' GGG TGG CGG CGC TGT GGT TGG CCA GGT
GCT GGC GGA TCG TCT CGG GGC TGC TCA CCT CGT TGC TGC TGA ACA
CGC TGG TGG GGC ACA GGA TCA CCT GGC CTC CGG CGT GC 3'

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FIGURE 19, CTD. 2/2

13856-307-2J (SEQ.ID.NO:75) 5' GCA GTT GAT CCG GCC CTT GTG GCT GCT
GTT GAA GGC GGT CAG GAT AGG GGC GCT GTC GAC GCT GTC GCG GTG
CAG CAG CTT GGT GGT GTG GCA GGG GTT GCC GGT GTC GGG 3'

13856-307-2L (SEQ.ID.NO:76) 5' CGT AGG TCA GGG TCA CGA TAG CGC TCT
TGT GCT TCA CGT TGT GGC CGG TCC AGT GCC AGG TGC TGC TCA CGG
CGG TGT ACA GCT TGC AGT GCT TCT TGA AGC GGT ACC GC 3'

13856-307-2M (SEQ.ID.NO:77) 5' TTT AGA TGC TCA TGA AGC CGG TGC TCA
CGG TGA TGG TCT TGG GGA TCT TCA CCT GGC TCA GGA ACT GGT CGC
GCT GCC ACT CGC TGT CGT AGG TCA GGG TCA CGA TAG CGC 3'

13856-307-2PA (SEQ.ID.NO:78) 5' CGA GCT GAT ATC GAA TTC AGA TCT GCC
ACC ATG GAG ACC CTG TGC CAG CG 3'

13856-307-2PM (SEQ.ID.NO:79) 5' GGT TGC AGA TCT AGA CTC GAG TTT AGA
TGC TCA TGA AGC CGG TGC 3'

13856-307-2PE (SEQ.ID.NO:80) 5' CCG GCT GCA TCA AGA AGC ACG 3'

13856-307-2PI (SEQ.ID.NO:81) 5' GGC CAA CCA CAG CGC CGC C 3'

13856-307-2PD (SEQ.ID.NO:82) 5' GCC GTG CTT CTT GAT GCA GCC 3'

13856-307-2PH (SEQ.ID.NO:83) 5' GGG TGG CGG CGC TGT GG 3'

13856-307-2PL (SEQ.ID.NO:84) 5' CGT AGG TCA GGG TCA CGA TAG C 3'

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001220-50121950

FIGURE 20

Oligonucleotides used in the generation of synthetic HPV 16 E7.

13856-307-7A (SEQ.ID.NO:85) 5'GGC CGG AGA TCT GAT ATC GAA TTC GCC
ACC ATG CAC GGC GAC ACC CCC ACC CTG CAC GAG TAC ATG CTG GAC
CTG CAG CCC GAG ACC ACC GAC CTG TAC GGC TAC GGC C 3'

13856-307-7C (SEQ.ID.NO:86) 5'GCC GAG CCC GAC CGC GCC CAC TAC AAC
ATC GTG ACC TTC TGC TGC AAG TGC GAC AGC ACC CTG CGC CTG TGC
GTG CAG AGC ACC CAC GTC GAC ATC CGC ACC CTG G 3'

13856-307-7B (SEQ.ID.NO:87) 5'GGG CGC GGT CGG GCT CGG CCT GGC CGG
CGG GGC CGT CGA TCT CGT CCT CTT CCT CGC TGC TGT CGT TCA GCT GGC
CGT AGC CGT ACA GGT CGG TGG 3'

13856-307-7D (SEQ.ID.NO:88) 5'CCG CGG CAG ATC TAG ACT CGA GTT TAG
GGC TTC TGG CTG CAG ATT GGG CAC ACG ATT CCC AGG GTG CCC ATC
AGC AGG TCC TCC AGG GTG CGG ATG TCG ACG TGG G 3'

13856-307-7PA (SEQ.ID.NO:89) 5'GGC CGG AGA TCT GAT ATC GAA TTC G 3'

13856-307-7PD (SEQ.ID.NO:90) 5'CCG CGG CAG ATC TAG ACT CG 3'

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FIGURE 21

Oligonucleotides Used for Construction of HPV6a E7 Gene

A. DNA Template Oligos

LS207 (105-mer) (SEQ.ID.NO:91) 5' GTC ACA GAT CTG ATA TCG AAT TCC ACC
ATG CAC GGC CGC CAC GTG ACC CTG AAG GAC ATC GTG CTG GAC CTG
CAG CCT CCC GAC CCC GTG GGC CTG CAC TGC TAC 3'

LS208 (105-mer) (SEQ.ID.NO:92) 5' CTG GAA GTG CTG CTT CAG GGG CTG GCT
GTC CTG GCC GTC CAC CTC GTC CAC CTC GTC GCT GTC CAC CAG
CTG CTC GTA GCA GTG CAG GCC CAC GGG GTC 3'

LS209 (107-mer) (SEQ.ID.NO:93) 5' CCA GCC CCT GAA GCA GCA CTT CCA GAT
CGT GAC CTG CTG CTG CGG CTG CGA CAG CAA CGT GCG CCT GGT GGT
GCA GTG CAC CGA GAC CGA CAT CCG CGA GGT GCA GC 3'

LS210 (102-mer) (SEQ.ID.NO:94) 5' CAG TCA GAT CTA GAG ATA TCT TTA GGT
CTT GGG AGC GCA GAT GGG GCA CAC GAT GTT CAG GGT ACC CAG CAG
GAG CTG CTG CAC CTC GCG GAT GTC GGT CTC 3'

B. PCR Amplification Primers

LS211 (24-mer) (SEQ.ID.NO:95) 5' GTC ACA GAT CTG ATA TCG AAT TCC 3'

LS212 (26-mer) (SEQ.ID.NO:96) 5' CAG TCA GAT CTA GAG ATA TCT TTA GG 3'

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FIGURE 22

Oligonucleotides Used for Construction of HPV18 E7 Gene

A. DNA Template Oligos

LS201 (109-mer) (SEQ.ID.NO:97) 5' GTC ACA GAT CTG ATA TCG AAT TCC ACC
ATG CAC GGC CCC AAG GCC ACC CTG CAG GAC ATC GTG CTG CAC CTG
GAG CCC CAG AAC GAG ATC CCC GTG GAC CTG CTG TGC C 3'

LS202 (111-mer) (SEQ.ID.NO:98) 5' GGG CTC GGC CCT GCG AGC GGG CAG
GTG CTG GTG GTT CAC GCC GTC GAT CTC GTC GTT CTC CTC CTC GCT GTC
GCT CAG CTG CTC GTG GCA CAG CAG GTC CAC GGG GAT CTC 3'

LS203 (108-mer) (SEQ.ID.NO:99) 5' GCC CGC TCG CAG GGC CGA GCC CCA
GCG CCA CAC CAT GCT GTG CAT GTG CTG CAA GTG CGA GGC CCG CAT
CGA GCT GGT GGT GGA GAG CAG CGC TGA CGA CCT GCG CGC 3'

LS204 (109-mer) (SEQ.ID.NO:100) 5' CAG TCA GAT CTA GAG ATA TCT TTA
CTG CTG GCT GGC GCA CCA GGG GCA CAC GAA GCT CAG GGT GTT CAG
GAA CAG CTG CTG GAA GGC GCG CAG GTC GTC AGC GCT GCT C 3'

B. PCR Amplification Primers

LS205 (26-mer) (SEQ.ID.NO:101) 5' GTC ACA GAT CTG ATA TCG AAT TCC AC
3'

LS206 (27-mer) (SEQ.ID.NO:102) 5' CAG TCA GAT CTA GAG ATA TCT TTA CTG
3'

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FIGURE 23

Oligonucleotides used in the construction of HPV6 E2

6A 1-84 (90mer) (SEQ.ID.NO:103) 5' GAA TTC AGA TCT GAT ATC ACC ATG
GAG GCC ATC GCC AAG CGC CTG GAC GCC TGC CAG GAG CAG CTG CTG
GAG CTG TAC GAG GAG AAC AGC 3'

6B 65-157 (92mer) (SEQ.ID.NO:104) 5' CCT TGT ACA GCA GCA CGC TCT
CGT GGC GCA TGC ACT TCC AGT GCA GCA CGT GCT TGT GCA GGT CGG
TGC TGT TCT CCT CGT ACA GCT CCA GC 3'

6C 132-227 (96mer) (SEQ.ID.NO:105) 5' CCA CGA GAG CGT GCT GCT GTA
CAA GGC CAA GCA GAT GGG CCT GAG CCA CAT CGG CAT GCA GGT GGT
GCC TCC TCT GAA GGT GAG CGA GGC CAA GGG 3'

6D 202-304 (103mer) (SEQ.ID.NO:106) 5' GCA GGG TCC AGG GCT CCA TGC
TGT ACT CGG TGC GCA GCA GGC TCT CGA GGT GCA TCT GCA TCT CGA
TGG CGT TGT GGC CCT TGG CCT CGC TCA CCT TCA GAG G 3'

6E 276-373 (98mer) (SEQ.ID.NO:107) 5' CGA GTA CAG CAT GGA GCC CTG
GAC CCT GCA GGA GAC CAG CTA CGA GAT GTG GCA GAC CCC TCC CAA
GCG CTG CTT CAA GAA GCG CGG CAA GAC CGT GG 3'

6F 347-448 (102mer) (SEQ.ID.NO:108) 5' CGT TGT CCT GCA CGT ACA CGT
CGG TCC ACA CCA CGT AGT CCA TGG TGT TGT TGG CGC AGC CGT CGA
ACT TCA CCT CCA CGG TCT TGC CGC GCT TCT TGA AGC 3'

6G 425-526 (102mer) (SEQ.ID.NO:109) 5' CCG ACG TGT ACG TGC AGG ACA
ACG ACA CCT GGG TGA AGG TGC ACA GCA TGG TGG ACG CCA AGG GCA
TCT ACT ACA CCT GTG GCC AGT TCA AGA CCT ACT ACG 3'

6H 495-586 (92mer) (SEQ.ID.NO:110) 5' GCT GCC GTA GCA CAC CTC CCA
GTG CTT GGT GCT GCC GTA CTT CTC GGC CTC CTT CAC GAA GTT CAC GTA
GTA GGT CTT GAA CTG GCC ACA GG 3'

6I 500-591 (94mer) (SEQ.ID.NO:111) 5' GCA CTG GGA GGT GTG CTA CGG
CAG CAC CGT GAT CTG CAG CCC CGC TAG CGT GAG CAG CAC CAC CCA
GGA GGT GAG CAT CCC CGA GAG CAC CAC C 3'

6J 636-732 (97mer) (SEQ.ID.NO:112) 5' GCG AGG AGG GGT CTG CAC GGC
GTC CTC CTT GGT GCT GCT GCT CAC CAG GGT GCT GGT CTG GGC GGG
AGT GTA GGT GGT GCT CTC GGG GAT GCT CAC C 3'

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FIGURE 23, CTD. 2/2

6K 708-804 (97mer) (SEQ.ID.NO:113) 5' GGA CGC CGT GCA GAC CCC TCC
TCG CAA GCG CGC CCG CGG CGT GCA GCA GAG CCC CTG CAA CGC CCT
GTG CGT GGC CCA CAT CGG CCC CGT GGA CAG C 3'

6L 780-873 (94mer) (SEQ.ID.NO:114) 5' GGC GCT GCT GTT GCT GTT GTT
GCG GCG CTG GTG CTG GTC GTG GTT GTT GGT GAT CAG GTT GTG GTT
GCC GCT GTC CAC GGG GCC GAT GTG GGC C 3'

6M 849-943 (95mer) (SEQ.ID.NO:115) 5' CCG CAA CAA CAG CAA CAG CAG
CGC CAC TCC CAT CGT GCA GTT CCA GGG CGA GAG CAA CTG CCT GAA
GTG CTT CCG CTA CCG CCT GAA CGA TCG CC 3'

6N 917-1012 (96mer) (SEQ.ID.NO:116) 5' CGT GCT TGT GGG GAG CCT TGC
TGC TGG CCC AGT GCC AGG TGC TGC TGA TCA GGT CGA ACA GGT GGC
GGT GGC GAT CGT TCA GGC GGT AGC GGA AGC 3'

6O 989-1083 (95mer) (SEQ.ID.NO:117) 5' GCA GCA AGG CTC CCC ACA AGC
ACG CCA TCG TGA CCG TGA CCT ACG ACA GCG AGG AGC AGC GCC AGC
AGT TCC TGG ACG TGG TGA AGA TCC CTC CC 3'

6P 1059-1154 (96mer) (SEQ.ID.NO:118) 5' CTC GAG AGA TCT CCC GGG TCT
AGA GCT TAC AGC AGG TGC AGG CTC ATG AAG CCC AGC TTG TGG CTG
ATG GTG GGA GGG ATC TTC ACC ACG TCC AGG 3'

6PA 25mer (SEQ.ID.NO:119) 5' GAA TTC AGA TCT GAT ATC ACC ATG G 3'

6PD 21mer (SEQ.ID.NO:120) 5' GCA GGG TCC AGG GCT CCA TGC 3'

6PE 25mer (SEQ.ID.NO:121) 5' CGA GTA CAG CAT GGA GCC CTG GAC C 3'

6PH 25mer (SEQ.ID.NO:122) 5' GCT GCC GTA GCA CAC CTC CCA GTG C 3'

6PI 21mer (SEQ.ID.NO:123) 5' GCA CTG GGA GGT GTG CTA CGG 3'

6PL 23mer (SEQ.ID.NO:124) 5' GGC GCT GCT GTT GCT GTT GTT GC 3'

6PM 22mer (SEQ.ID.NO:125) 5' CCG CAA CAA CAG CAA CAG CAG C 3'

6PP 26mer (SEQ.ID.NO:126) 5' CTC GAG AGA TCT CCC GGG TCT AGA GC 3'

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[illegible]

18A 1-97 (97mer) (SEQ.ID.NO:127) 5' GAA TTC AGA TCT GAT ATC ACC ATG
CAG ACT CCC AAG GAG ACC CTG AGC GAG CGC CTG AGC GCC CTG CAG
GA CAA GAT CAT CGA CCA CTA CGA GAA CG 3'

18B 69-166 (98mer) (SEQ.ID.NO:128) 5' CGA AGA AGA TGG CGT TCT CCC
AGC GGA TCA GCT GCC AGT ACT GGA TCT GGC TGT CGA TGT CCT TGC
TGT CGT TCT CGT AGT GGT CGA TGA TCT TGT CC 3'

18C 141-234 (94mer) (SEQ.ID.NO:129) 5' CCG CTG GGA GAA CGC CAT CTT
CTT CGC CGC TCG CGA GCA CGG GAT CCA GAC CCT GAA CCA CCA GGT
GGT GCC CGC CTA CAA CAT CAG CAA GAG C 3'

18D 211-304 (94mer) (SEQ.ID.NO:130) 5' CCT CGG TCT TGT AGG CGC TCT
GGG CCA GGC CCT GCA GGG CCA TCT GCA GCT CGA TGG CCT TGT GGG
CCT TGC TCT TGC TGA TGT TGT AGG CGG G 3'

18E 281-371 (91mer) (SEQ.ID.NO:131) 5'CCC AGA GCG CCT ACA AGA CCG
AGG ACT GGA CCC TGC AGG ACA CCT GCG AGG AGC TGT GGA ACA CCG
AGC CCA CCC ACT GCT TCA AGA AGG G 3'

18F 348-441 (94mer) (SEQ.ID.NO:132) 5' GCT GTC CCA GGC CAC GTA GTT
CAT GCA GTT GTC CTT GTT GCC GTC GAA GTA CAC CTG CAC GGT CTG
GCC TCC CTT CTT GAA GCA GTG GGT GGG C 3'

18G 416-505 (90mer) (SEQ.ID.NO:133) 5'GCA TGA ACT ACG TGG CCT GGG
ACA GCG TGT ACT ACA TGA CCG ACG CCG GCA CCT GGG ACA AGA CCG
CCA CCT GCG TGA GCC ACC GCG GCC 3'

18H 481-572 (92mer) (SEQ.ID.NO:134) 5' CCG TAC TTC TCG CAC TCG CTC
TTG AAC TCG ATG TAG AAG GTG TTG TAG CCC TCC TTC ACG TAG TAC
AGG CCG CGG TGG CTC ACG CAG GTG GC 3'

18I 543-636 (94mer) (SEQ.ID.NO:135) 5'CGA GTT CAA GAG CGA GTG CGA
GAA GTA CGG CAA CAC CGG CAC CTG GGA GGT GCA CTT CGG CAA CAA
CGT GAT CGA CTG CAA CGA CAG CAT GTG C 3'

18J 609-708 (100mer) (SEQ.ID.NO:136) 5' GCT GTA GGG GCT GGG AGT GTG
CTG CAG CTG CTT CAC CAG CTG GGT GGC GCT CAC GGT GTC GTC GCT
GGT GCT GCA CAT GCT GTC GTT GCA GTC GAT CAC G 3'

Figure 1 is a schematic representation of the experimental design. It shows a flow from 'Study 1' to 'Study 2'. Study 1 involves 'Pre-Test' and 'Post-Test' with 'Control' and 'Intervention' groups. Study 2 involves 'Pre-Test' and 'Post-Test' with 'Control' and 'Intervention' groups. The 'Intervention' group in Study 2 is further divided into 'Intervention 1' and 'Intervention 2'.

18L 758-853 (96mer) (SEQ.ID.NO:138) 5' GCT TGT TGT TGC CGG TGG CGG
TGG CGG CGC CCA GCA GAG GGT TCA CGG GCC CGC AGT GCT GCT TCT
CGG CCA GGC CGC AGT GGC CAG GGC GAG TGG 3'

18M 829-925 (97mer) (SEQ.ID.NO:139) 5'GCC ACC GCC ACC GGC AAC AAC
AAG CGC CGC AAG CTG TGC AGC GGC AAC ACC ACT CCC ATC ATC CAC
CTG AAG GGC GAC CGC AAC AGC CTG AAG TGC C 3'

18N 900-996 (97mer) (SEQ.ID.NO:140) 5' GGC GCC GGT CCA GTG CCA GGT
GCT GCT GAT GTC GCG GTA GTG GTC GCT GTG CTT GCG CAG GCG GTA
CCG CAG GCA CTT CAG GCT GTT GCG GTC GCC C 3'

180 974-1072 (99mer) (SEQ.ID.NO:141) 5' GCA CCT GGC ACT GGA CCG GCG
CCG GGA ACG AGA AGA CCG GCA TCC TGA CCG TGA CCT ACC ACA GCG
AGA CCC AGC GCA CCA AGT TCC TGA ACA CCG TGG 3'

18P 1048-1145 (98mer) (SEQ.ID.NO:142) 5' CTC GAG AGA TCT CCC GGG TCT
AGA GCT TAC ATG GTC ATG TAG CCC ACC AGG ATC TGC ACG CTG TCG
GGG ATG GCC ACG GTG TTC AGG AAC TTG GTG CG 3'

18PA 25mer (SEQ.ID.NO:143) 5'GAA TTC AGA TCT GAT ATC ACC ATG C 3'

18PD 23mer (SEQ.ID.NO:144) 5' CCT CGG TCT TGT AGG CGC TCT GG 3'

18PE 21mer (SEQ.ID.NO:145) 5' CCC AGA GCG CCT ACA AGA CCG 3'

18PH 21mer (SEQ.ID.NO:146) 5' CCG TAC TTC TCG CAC TCG CTC 3'

18PI 20mer (SEQ.ID.NO:147) 5' CGA GTT CAA GAG CGA GTG CG 3'

18PL 21mer (SEQ.ID.NO:148) 5' GCT TGT TGT TGC CGG TGG CGG 3'

18PM 25mer (SEQ.ID.NO:149) 5'GCC ACC GCC ACC GGC AAC AAC AAG C 3'

18PP 26mer (SEQ.ID.NO:150) 5' CTC GAG AGA TCT CCC GGG TCT AGA GC 3'

FIGURE 25

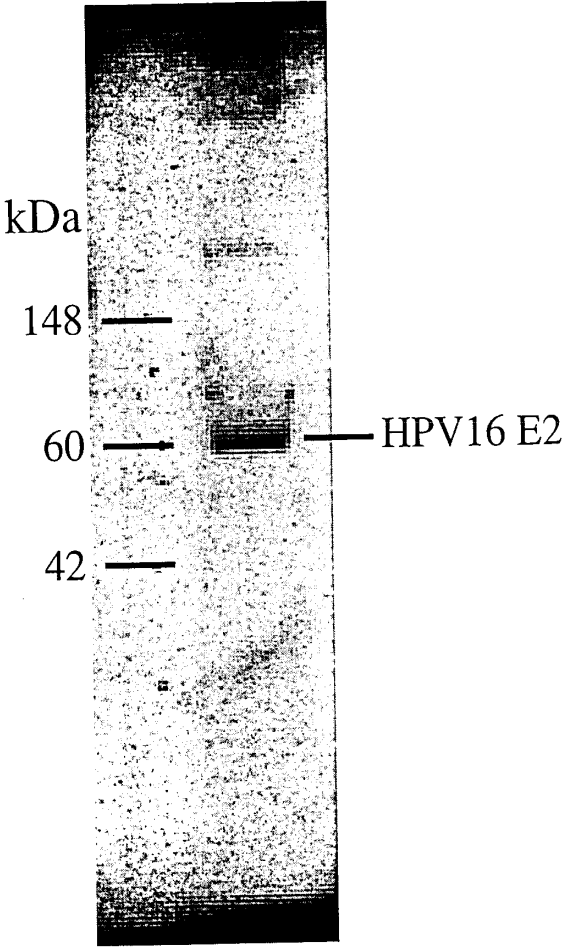
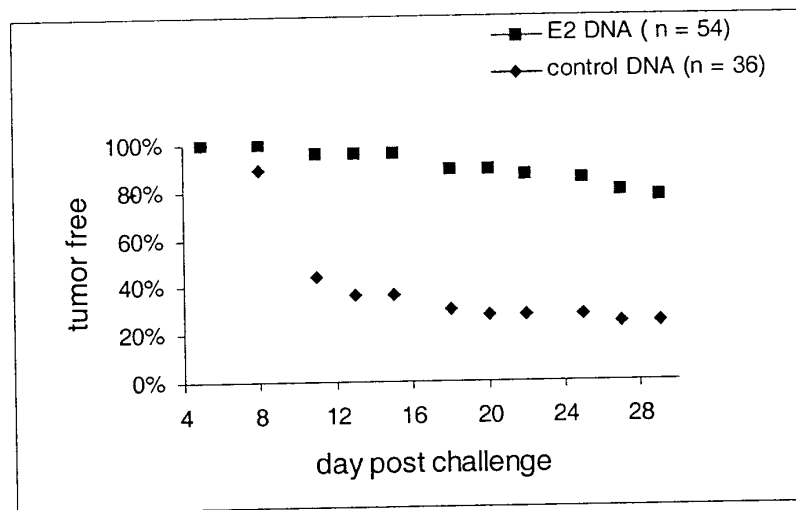


FIGURE 26



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